



#8

SEQUENCE LISTING

<110> BONNEFOY, Jean-Yves Marcel Paul
CROWE, James Scott
ELLIS, Jonathan Henry
RAPSON, Nicholas Timothy
SHEARIN, Jean

<120> Antibodies to CD23, derivatives thereof, and their therapeutic uses

<130> 1430-256/PG3433US

<140> US 09/674,716

<141> 2001-01-22

<150> CA 2,328,606

<151> 1999-05-07

<150> PCT/GB99/01434

<151> 1999-05-07

<150> GB 9809839.5

<151> 1998-05-09

<160> 53

<170> PatentIn Ver. 2.1

<210> 1

<211> 415

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (3)..(413)

<400> 1

aa gct tta cag tta ctc agc aca cag gac ctc acc atg gat ttt ggg 47
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly
1 5 10 15

ctg att ttt ttt att gtt ctt tta aaa ggg gtc cag agt gaa gtg aag 95
Leu Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys
20 25 30

ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga tcc atg aaa 143
Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys
35 40 45

ctc tcc tgt gta gcc tct gga ttt act ttc agt ggc tac tgg atg tct 191
Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser
50 55 60

tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt gct gaa att 239
Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile
65 70 75

aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct gtg aaa 287
 Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys
 80 85 90 95

ggg aag ttc acc atc tca aga gat gat tcc aaa agt cgt ctc tac ctg 335
 Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu
 100 105 110

caa atg aac agc tta aga gct gaa gac agt gga gtt tat tac tgt aca 383
 Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr
 115 120 125

gat ttc ata gac tgg ggc caa ggg aca cta gt 415
 Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu
 130 135

<210> 2
 <211> 437
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (3)..(437)

<400> 2
 aa gct tta cag tta ctc agc aca cag gac ctc acc atg agg ttc tct 47
 Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser
 1 5 10 15

gtt cag ttt ctg ggg gtg ctt atg ttc tgg atc tct gga gtc agt ggg 95
 Val Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly
 20 25 30

gat att gtg ata acc cag gat gaa ctc tcc aat cct gtc act tct gga 143
 Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly
 35 40 45

gaa tca gtt tcc atc tcc tgc agg tct agt aag agt ctc ctg tat aag 191
 Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 50 55 60

gat ggg aag aca tac ttg aat tgg ttt ctg cag aga cca gga caa tct 239
 Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
 65 70 75

cct cag ctc ctg atg tat ttg atg tcc acc cgt gca tca gga gtc tca 287
 Pro Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser
 80 85 90 95

gac cgg ttt agt ggc agt ggg tca ggc aca gat ttc acc ctg gaa atc 335
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
 100 105 110

agt aga gtg aag gct gag gat gtg ggt gtg tat tac tgt caa caa ctt 383
 Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 115 120 125

gta gag tat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa 431
 Val Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 130 135 140

cgt acg 437
 Arg Thr
 145

<210> 3
 <211> 16
 <212> PRT
 <213> Mus musculus

<400> 3
 Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn
 1 5 10 15

<210> 4
 <211> 48
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(48)

<400> 4
 cgc tcg agt aag agt ctc ctg tat aag gat ggg aag aca tac ttg aat 48
 Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp Gly Lys Thr Tyr Leu Asn
 1 5 10 15

<210> 5
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 5
 Leu Met Ser Thr Arg Ala Ser
 1 5

<210> 6
 <211> 21
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(21)

<400> 6
 ttg atg tcc acc cgg gca tca 21
 Leu Met Ser Thr Arg Ala Ser
 1 5

<210> 7
<211> 9
<212> PRT
<213> Mus musculus

<400> 7
Gln Gln Leu Val Glu Tyr Pro Phe Thr
1 5

<210> 8
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 8
caa cag ctg gta gag tat cca ttc acg
Gln Gln Leu Val Glu Tyr Pro Phe Thr
1 5

27

<210> 9
<211> 5
<212> PRT
<213> Mus musculus

<400> 9
Gly Tyr Trp Met Ser
1 5

<210> 10
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 10
ggc tac tgg atg tcc

15

<210> 11
<211> 19
<212> PRT
<213> Mus musculus

<400> 11
Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Thy Ala Glu Ser
1 5 10 15

Val Lys Gly

<210> 12
<211> 57
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(57)

<400> 12
gaa att aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct 48
Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser
1 5 10 15

gtg aag ggg 57
Val Lys Gly

<210> 13
<211> 3
<212> PRT
<213> Mus musculus

<400> 13
Phe Ile Asp

<210> 14
<211> 9
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(9)

<400> 14
ttc ata gac 9
Phe Ile Asp

<210> 15
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic sequence

<400> 15
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser

<210> 16
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic sequence

<400> 16
 Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
 1 5 10 15

Ala Gln Ala

<210> 17
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Humanised anti-CD23 antibody light chain variable region

<220>
 <221> CDS
 <222> (1)..(348)

<400> 17
 gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct gga 48
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

gag ccg gcc tcc atc tcc tgt cgc tcg agt aag agt ctc ctg tat aag 96
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
 20 25 30

gat ggg aag aca tac ttg aat tgg tac ctg cag aag cca ggg cag tct 144
 Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

cca cag ctc ctg atc tat ttg atg tcc acc cgg gca tca ggg gtc cct 192
 Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
 50 55 60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgt caa cag ctg 288
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
 85 90 95

gta gag tat cca ttc acg ttc ggc caa ggg acc aag gtg gag atc aaa 336
Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

cgt acg gtg gct 348
Arg Thr Val Ala
115

<210> 18
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Humanised anti-CD23 antibody heavy chain variable region.

<220>
<221> CDS
<222> (1)..(1335)

<400> 18
gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag ccc ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

tcc ctt aga ctc tcc tgt gca gct agc gga ttc act ttc agt ggc tac 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

tgg atg tcc tgg gtc cgc cag gct cca ggg aag ggg ctc gag tgg gtt 144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gct gaa att aga ttg aaa tct gat aat tat gca aca cat tat gcg gag 192
Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

tct gtg aag ggg aaa ttc acc atc tca aga gat gat tca aaa tct aga 240
Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg
65 70 75 80

ctg tat ctg caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat 288
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

tac tgt aca gat ttc ata gac tgg ggc cag gga aca cta gtc acc gtc 336
Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 384
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag 432
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg	480
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
145 150 155 160	
acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	528
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
165 170 175	
tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	576
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
180 185 190	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	624
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
195 200 205	
gac aag aaa gtg gag ccc aaa tct tgt gac aaa act cac aca tgc cca	672
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
210 215 220	
ccg tgc cca gca cct gaa ctc gcg ggg gca ccg tca gtc ttc ctc ttc	720
Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe	
225 230 235 240	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	768
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
245 250 255	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	816
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
260 265 270	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	864
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
275 280 285	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	912
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
290 295 300	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	960
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
305 310 315 320	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1008
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
325 330 335	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg	1056
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
340 345 350	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1104
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
355 360 365	

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1152
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
370 375 380	

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1200
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
385 390 395 400	

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag	1248
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
405 410 415	

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac	1296
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
420 425 430	

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1335
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
435 440	

<210> 19
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 19	
gatgaagctt tacagttact cagcacacag gacctcacca tggattttgg gctgatt	57

<210> 20
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 20	
gatggactag tgtcccttgg cccca	25

<210> 21
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo

<400> 21	
gatgaagctt tacagttact cagcacacag gacctcacca tgaggttctc tgttcag	57

<210> 22
 <211> 28
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 22
gatgcgtacg tytkatytcc avcttkgt 28

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 23
gatcaagctt ctctacagtt actgagcaca 30

<210> 24
<211> 63
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 24
aatcaagtat gtcttcccat ccttatacag gagactctta ctcgagcgac aggagatgga 60
ggc 63

<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 25
cgctcgagta agagtctcct gtataaggat gggaagacat acttgaattg gtacctgcag 60
aag 63

<210> 26
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 26
tgatgccgg gtggacatca aatagatcag gagctg 36

<210> 27
<211> 36
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 27

ttgatgtcca cccgggcatc aggggtccct gacagg 36

<210> 28

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 28

agccacctga cgtttgatct ccaccttggt cccttggccg aacgtgaatg gatactctac 60
cagctgttga cagtaataaa cccc 84

<210> 29

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 29

acacgaagct tcaccatggc ttgggtgtgg accttgctat tcctgatggc ggccgcccaa 60

<210> 30

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 30

ctttaccaag cctccccag actccaccag ctgcacctct gcttgggcac tttgggcggc 60
cgccat 66

<210> 31

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 31

ttggtaaagc ccgggggggc ccttagactc tcctgtgcag ctagcggatt cactttcagt 60

<210> 32

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 32

ccccttccct ggagcctggc ggacccagga catccagtag ccaactgaaag tgaatccgct 60

<210> 33

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 33

gggaaggggc tcgagtgggt tgctgaaatt agattgaaat ctgataatta tgcaacacat 60

<210> 34

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 34

atcatctctt gagatgggtga atttcccctt cacagactcc gcataatgtg ttgcataatt 60

<210> 35

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 35

atctcaagag atgattcaaa atctagactg tatctgcaaa tgaacagcct gaaaaccgag 60
gacaca 66

<210> 36

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 36

ggtgactagt gttccctggc cccagtctat gaaatctgta cagtaatata cggctgtgtc 60
ctcggtttt 69

<210> 37

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 37
gctgctcctt ttaagctttg gggtaagggc tcactagtca cagtctcc 48

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 38
tgacgggtgcc cccgcgagtt cagg 24

<210> 39
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 39
cctgaactcg cgggggcacc gtca 24

<210> 40
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo

<400> 40
aagcttcggt cgaattcatt tacccggaga cag 33

<210> 41
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41
actagtcgac atgaagtttc cttctcaact tctgctc 37

<210> 42
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic sequence

<400> 42
 Thr Lys Leu Glu Ile Lys Arg Thr
 1 5

<210> 43
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic sequence

<400> 43
 Thr Lys Val Glu Ile Lys Arg Thr
 1 5

<210> 44
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic sequence

<400> 44
 Thr Lys Leu Glu Ile Arg Arg Thr
 1 5

<210> 45
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic sequence

<400> 45
 Thr Lys Val Glu Ile Arg Arg Thr
 1 5

<210> 46
 <211> 415
 <212> DNA
 <213> Mus musculus

<400> 46
 actagtgtcc cttggcccca gtctatgaaa tctgtacagt aataaactcc actgtcttca 60
 gctcttaagc tgttcatttg caggtagaga cgacttttgg aatcatctct tgagatgggtg 120
 aacttcctt tcacagactc cgcataatgt gttgcataat tatcagattt caatctaatt 180

```

tcagcaaccc actcaagccc cttctctgga gactggcgga cccaagacat ccagtagcca 240
ctgaaagtaa atccagaggc tacacaggag agtttcatgg atcctccagg ttgcaccaag 300
cctcctccag actcctcaag cttcacttca ctctggaccc cttttaaaag aacaataaaa 360
aaaatcagcc caaaatccat ggtgaggtcc tgtgtgctga gtaactgtaa agctt 415

```

```

<210> 47
<211> 437
<212> DNA
<213> Mus musculus

```

```

<400> 47
cgtacgtttt atttccaact ttgtccccga gccgaacgtg aatggatact ctacaagttg 60
ttgacagtaa tacacacca catcctcagc cttcactcta ctgatttcca gggtgaaatc 120
tgtgcctgac ccactgccac taaaccggtc tgagactcct gatgcacggg tggacatcaa 180
atacatcagg agctgaggag attgtcctgg tctctgcaga aaccaattca agtatgtctt 240
cccactctta tacaggagac tcttactaga cctgcaggag atggaaactg attctccaga 300
agtgcagga ttggagagtt catcctgggt tatcacaata tccccactga ctccagagat 360
ccagaacata agcaccacca gaaactgaac agagaacctc atggtgaggt cctgtgtgct 420
gagtaactgt aaagctt 437

```

```

<210> 48
<211> 348
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Humanised anti-CD23 antibody light
chain variable region

```

```

<400> 48
agccaccgta cgtttgatct ccaccttggc ccttggccg aacgtgaatg gatactctac 60
cagctgttga cagtaataaa cccaacatc ctcagcctcc actctgctga ttttcagtgt 120
aaaatctgtg cctgatccac tgccactgaa cctgtcaggg acccctgatg cccgggtgga 180
catcaaatag atcaggagct gtggagactg ccttggcttc tgcaggatcc aattcaagta 240
tgtcttccca tccttatata ggagactctt actcgagcga caggagatgg aggccggctc 300
tccaggggtg acgggcaggg agagtggaga ctgagtcac acaatatc 348

```

```

<210> 49
<211> 1335
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Humanised anti-CD23 antibody heavy
chain variable region

```

```

<400> 49
tcatttaccc ggagacaggg agaggctctt ctgcgtgtag tggttgtgca gagcctcatg 60
catcacggag catgagaaga cgttcccctg ctgccacctg ctcttgtcca cggtagactt 120
gctgtagagg aagaaggagc cgtcggagtc cagcacggga ggcgtggtct tgtagtgtgt 180
ctccggctgc ccattgctct cccactccac ggcgatgtcg ctgggataga agcctttgac 240
caggcaggtc aggtgacct ggttcttggc cagctcatcc cgggatgggg gcagggtgta 300
cacctgtggt tctcggggct gccctttggc tttggagatg gttttctcga tgggggctgg 360
gagggctttg ttggagacct tgcacttgta ctccttgcca ttcagccagt cctggtgcag 420
gacggtgagg acgtgacca cacggtacgt gctgttgtag tgctcctccc gcggctttgt 480
cttggcatta tgcacctcca cgccgtccac gtaccagttg aacttgacct cagggtcttc 540
gtggctcacg tccaccacca cgcagtgtgc ctcaggggtc cgggagatca tgagggtgtc 600

```

```

cttgggtttt ggggggaaga ggaagactga cgggtgcccc gcgagttcag gtgctgggca 660
cgggtgggcat gtgtgagttt tgtcacaaga tttgggctcc actttcttgt ccaccttggt 720
gttgctgggc ttgtgattca cgttgagat gtaggtctgg gtgccaagc tgctggaggg 780
cacggtcacc acgctgctga gggagtagag tcctgaggac tgtaggacag ccgggaaggt 840
gtgcacgccg ctggtcaggg cgcctgagtt ccacgacacc gtcaccggtt cggggaagta 900
gtccttgacc aggcagccca gggccgctgt gccccagag gtgctcttgg aggaggggtgc 960
cagggggaag accgatgggc ccttggtgga ggctgaggag acggtgacta gtgttccttg 1020
gccccagtct atgaaatctg tacagtaata cacggctgtg tcctcggttt tcaggctgtt 1080
catttgcaga tacagtctag attttgaatc atctcttgag atggtgaatt tccccctcac 1140
agactccgca taatgtgttg cataattatc agatttcaat ctaatttcag caaccactc 1200
gagccccctt cctggagcct ggcggaccca ggacatccag tagccactga aagtgaatcc 1260
gctagctgca caggagagtc taagggaccc cccgggcttt accaagcctc cccagactc 1320
caccagctgc acctc                                     1335

```

<210> 50
 <211> 137
 <212> PRT
 <213> Mus musculus

```

<400> 50
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly Leu
  1              5              10              15

Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys Leu
      20              25              30

Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu
      35              40              45

Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser Trp
      50              55              60

Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg
      65              70              75              80

Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys Gly
      85              90              95

Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu Gln
      100             105             110

Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr Asp
      115             120             125

Phe Ile Asp Trp Gly Gln Gly Thr Leu
      130             135

```

<210> 51
 <211> 145
 <212> PRT
 <213> Mus musculus

```

<400> 51
Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser Val
  1              5              10              15

Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly Asp

```


	20		25		30
Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly Glu	35	40	45		
Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp	50	55	60		
Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro	65	70	75	80	
Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser Asp	85	90	95		
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile Ser	100	105	110		
Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu Val	115	120	125		
Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg	130	135	140		

Thr
145

<210> 52

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised anti-CD23 antibody light chain variable region

<400> 52

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly	1	5	10	15
---	---	---	----	----

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys	20	25	30
---	----	----	----

Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser	35	40	45
---	----	----	----

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro	50	55	60
---	----	----	----

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	65	70	75	80
---	----	----	----	----

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu	85	90	95
---	----	----	----

Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	100	105	110
---	-----	-----	-----

Arg Thr Val Ala
115

<210> 53

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised anti-CD23 antibody heavy chain variable region

<400> 53

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 340 345 350
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 355 360 365
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 370 375 380
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 385 390 395 400
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 405 410 415
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 420 425 430
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440
